

## RAW SEQUENCE LISTING

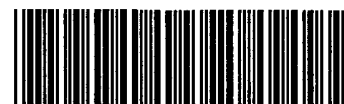
The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/661,399

Source: IFWO

Date Processed by STIC: 11/5/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 11/05/2004

PATENT APPLICATION: US/10/661,399

TIME: 12:27:17

Input Set : A:\1200029-US2.ST25.txt

Output Set : N:\CRF4\11052004\J661399.raw

(p3.6)

3 &lt;110&gt; APPLICANT: Soll, Dieter

5 &lt;120&gt; TITLE OF INVENTION: GlutRNAGLN AMIDOTRANSFERASE - A NOVEL ESSENTIAL

## TRANSLATIONAL

6 COMPONENT

8 &lt;130&gt; FILE REFERENCE: 03818/1200029-US2

10 &lt;140&gt; CURRENT APPLICATION NUMBER: 10/661,399

11 &lt;141&gt; CURRENT FILING DATE: 2003-09-12

13 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/037,275

14 &lt;151&gt; PRIOR FILING DATE: 1997-02-03

16 &lt;150&gt; PRIOR APPLICATION NUMBER: PCT/US98/01860

17 &lt;151&gt; PRIOR FILING DATE: 1998-02-03

19 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/355,622

20 &lt;151&gt; PRIOR FILING DATE: 1999-09-23

22 &lt;160&gt; NUMBER OF SEQ ID NOS: 8

24 &lt;170&gt; SOFTWARE: PatentIn version 3.2

26 &lt;210&gt; SEQ ID NO: 1

27 &lt;211&gt; LENGTH: 3495

28 &lt;212&gt; TYPE: DNA

29 &lt;213&gt; ORGANISM: Bacillus subtilis

32 &lt;220&gt; FEATURE:

33 &lt;221&gt; NAME/KEY: misc\_feature

34 &lt;222&gt; LOCATION: (2330)..(2330)

35 &lt;223&gt; OTHER INFORMATION: n is a, c, g, or t

37 &lt;220&gt; FEATURE:

38 &lt;221&gt; NAME/KEY: misc\_feature

39 &lt;222&gt; LOCATION: (2365)..(2365)

40 &lt;223&gt; OTHER INFORMATION: n is a, c, g, or t

42 &lt;400&gt; SEQUENCE: 1

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45	gtattatatg	acttaacgga	gaaatatgtg	gaggtggatc	atatgtcacg	aatttcaata	120
47	gaagaagtaa	agcacgttgc	gcaccttgca	agacttgcca	ttactgaaga	agaagcaaaa	180
49	atgttcaactg	aacagctcga	cagtatcatt	tcatttgccg	aggagcttaa	tgaggttaac	240
51	acagacaatg	tggagcctac	aactcacgtg	ctgaaaatga	aaaatgtcat	gagagaagat	300
53	gaagcgggta	aaggtcttcc	ggttgaggat	gtcatgaaaa	atgcgcctga	ccataaagac	360
55	ggctatatte	gtgtgccatc	aattctggac	taaaggaggg	acacaagaat	gtcattattt	420
57	gatcataaaa	tcacagaatt	aaaacagctc	atacataaaa	aagagattaa	gattttctgat	480
59	ctgggttgatg	aattcttataa	acgcattcaa	gcggttgatg	ataaggatca	agcctttttg	540
61	gcattagatg	aagaaagagc	gcgcgcatac	gcgaaggagc	ttgatgaggc	ggttgacggc	600
63	cgtttctgagc	acggtcttct	tttcgggatg	cccacggcg	taaaagataa	tatcgtaaca	660
65	aaagggctgc	gcacaacatg	ctccagcaaa	attctcgaaa	actttgatcc	gatttacgat	720
67	gctactgtcg	ttcagcgctt	tcaagacgct	gaagcgggtc	caatcgga	actgaacatg	780
69	gacgaattcg	ccatgggggtc	atctacagaa	aactcagctt	acaagctgac	gaaaaaccct	840
71	tggaaactgg	atacagttcc	cggcggttca	agcggcggat	ctgcagctgc	ggttgctgcg	900
73	ggagaagtcc	cgttttctct	tggatctgac	acaggcggct	ccatccgtca	gccggcatct	960

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75 ttctgcgccg ttgtcggatt aaaacctaca tacggacgtg tatctcggtta cggcctggtc 1020
77 gcatttgccg cttcattgga ccaaactcga cgcattacac gtacgggtga ggataacgcg 1080
79 tttttacttc aagcgatttc cggcgtagac aaaatggact ctacgagtgc aaatgtggac 1140
81 gtgectgatt ttctttcttc attaaactggc gacatcaaag gactgaaaat cgcggttccg 1200
83 aaagaatacc ttggtgaagg tgtcggcaaa gaagcgagag aatctgtctt ggcagcgctg 1260
85 aaagtccttg aaggtctcgg cgctacatgg gaagaagtgt ctcttcgca cagtaaatac 1320
87 gcgcttgcca catattacct gctgtcatct tctgaagcgt cagcgaaact tgcacgcttt 1380
89 gacggcatcc gctacggcta ccgcacagac aacgcggata acctgatcga cttttacaag 1440
91 caaacgcgcg ctgaagggtt cggaatgaa gtcaaacgcc gcacatgct cggaacgttt 1500
93 gctttaagct caggctacta cgatgcgtac taaaaaaaag cgaaaaaagt gcgtacgttg 1560
95 attaagaagg atttcgagga cgtatttgaa aaatatgatg ttattgttgg accgactaca 1620
97 ccgacacctg cgtttaaaat cggtgaaaac acgaaggatc cgctcacaat gtacgcaaac 1680
99 gatattctaa cgattccggg caaccttgcg gcgtaccggg aatcaggtgc catgcggtta 1740
101 gcagacggac ttccgctcgg cctgcaaatc atcggaaaac actttgatga agcactgtat 1800
103 accgcgttgc tcatgcattt gaacaagcaa cagaccatca taaagcaaaa cctgaactgt 1860
105 aaggggtgaa agaattgaa ctttgaaacg gtaatcggac ttgaagtcca cgttgagtta 1920
107 aaaacaaaat caaaaatttt ctcaagctct ccaacgccat tcggcgcgga ggcgaatacg 1980
109 cagacaagcg ttattgacct cggatatccg ggcgtcctgc ctggtctgaa caaagaagcc 2040
111 gttgaattcg caatgaaagc cgctatggcg ctcaactgtg agatcgcaac ggatacgaag 2100
113 tttagaccga aaaactattt ctatcctgac aaccgaaaag cgtatcagat ttctcaattt 2160
115 gataagccaa tcggcgaaaa cggctggatc gaaattgaag tcggcggaac aacaaaacgc 2220
117 atcggcatca cgcgccttca tcttgaagag gatgcgggaa aactgacgca tacgggcgac 2280
W--> 119 ggctattctc ttgttgactt caaccgtcaa ggaacgcgcg ttgttgagtn cgtatcagag 2340
121 ccggacatcc gcacgcgga agaancgtac gcatacttg aaaagctgaa atccatcatc 2400
123 caatatacag gcgtttctga ctgtaaaatg gaagaaggct cacttcgctg tgacgccaat 2460
125 atctctcttc gtccgatcgg ccaagaggaa ttcggcacia aaacagaatt gaaaaacttg 2520
127 aactcctttg cgtttgttca aaaaggcctt gagcatgaag aaaaacgcca ggagcaggtt 2580
129 cttcttttcg gcttcttcat ccagcaagaa actcgccgtt atgatgaagc aacgaagaaa 2640
131 accattctta tgcgtgtcaa agagggatct gacgactacc gttactttcc agagccagat 2700
133 ctagtccgac tctacattga tgatgaatgg aaggaacgcg taaaagcaag cattcctgag 2760
135 cttccggatg agcgcgcaa gcgttatatc gaagagcttg gcttcgctgc atatgacgca 2820
137 atggttctga cgtgacaaa agaaatggct gatttcttcg aagaaaccgt tcaaaaaggc 2880
139 gctgaagcta aacaagcgtc taactggctg atgggtgaag tgtcagctta cctaaacgca 2940
141 gaacaaaaag agcttgccga tgttgccctg acacctgaag gccttgccgg catgatcaaa 3000
143 ttgattgaaa aaggaacctt ttcttctaag atcgcgaaag aagtgtttaa agaattgatt 3060
145 gaaaaaggcg gcgacgctga gaagattgtg aaagagaaag gccttgttca gatttctgac 3120
147 gaaggcgtgc ttctgaagct tgtcactgag gcgcttgaca acaatcctca atcaatcgaa 3180
149 gactttaaaa acggaaaaga ccgcgcgatc ggcttccctg tcggacagat tatgaaagcg 3240
151 tccaaaggac aagccaaccc gccgatggtc aacaaaattc tgcttgaaga aattaaaaaa 3300
153 cgctaataaa aaagcagccc ttagaggctg ctttttttat ggtcaaattg agataaagac 3360
155 aagatgaggg cccgaagcct ttcaacttct ttgtcgttgg ttccggccaa attggacagc 3420
157 atgcctttat aatcggcttg cgcggtttat cctgagtcaa ttcttcctcg ataagataag 3480
159 tgacacggtg atatc 3495

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162 &lt;210&gt; SEQ ID NO: 2

163 &lt;211&gt; LENGTH: 1155

164 &lt;212&gt; TYPE: PRT

165 &lt;213&gt; ORGANISM: Bacillus subtilis

168 &lt;220&gt; FEATURE:

169 &lt;221&gt; NAME/KEY: misc\_feature

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Input Set : A:\1200029-US2.ST25.txt

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170 <222> LOCATION: (774)..(774)
171 <223> OTHER INFORMATION: Xaa is Phe, Ser, Tyr, or Cys
173 <220> FEATURE:
174 <221> NAME/KEY: misc_feature
175 <222> LOCATION: (786)..(786)
176 <223> OTHER INFORMATION: Xaa is Ser, Pro, Thr, or Ala
178 <400> SEQUENCE: 2
180 Glu Phe Asp Pro Val Ser Arg Arg Phe Val Ala Leu Lys Gly Leu Phe
181 1 5 10 15
184 Leu Ile Ser Val Leu Tyr Asp Leu Thr Glu Lys Tyr Val Glu Val Asp
185 20 25 30
188 His Met Ser Arg Ile Ser Ile Glu Glu Val Lys His Val Ala His Leu
189 35 40 45
192 Ala Arg Leu Ala Ile Thr Glu Glu Glu Ala Lys Met Phe Thr Glu Gln
193 50 55 60
196 Leu Asp Ser Ile Ile Ser Phe Ala Glu Glu Leu Asn Glu Val Asn Thr
197 65 70 75 80
200 Asp Asn Val Glu Pro Thr Thr His Val Leu Lys Met Lys Asn Val Met
201 85 90 95
204 Arg Glu Asp Glu Ala Gly Lys Gly Leu Pro Val Glu Asp Val Met Lys
205 100 105 110
208 Asn Ala Pro Asp His Lys Asp Gly Tyr Ile Arg Val Pro Ser Ile Leu
209 115 120 125
212 Asp Arg Arg Asp Thr Arg Met Ser Leu Phe Asp His Lys Ile Thr Glu
213 130 135 140
216 Leu Lys Gln Leu Ile His Lys Lys Glu Ile Lys Ile Ser Asp Leu Val
217 145 150 155 160
220 Asp Glu Ser Tyr Lys Arg Ile Gln Ala Val Asp Asp Lys Val Gln Ala
221 165 170 175
224 Phe Leu Ala Leu Asp Glu Glu Arg Ala Arg Ala Tyr Ala Lys Glu Leu
225 180 185 190
228 Asp Glu Ala Val Asp Gly Arg Ser Glu His Gly Leu Leu Phe Gly Met
229 195 200 205
232 Pro Ile Gly Val Lys Asp Asn Ile Val Thr Lys Gly Leu Arg Thr Thr
233 210 215 220
236 Cys Ser Ser Lys Ile Leu Glu Asn Phe Asp Pro Ile Tyr Asp Ala Thr
237 225 230 235 240
240 Val Val Gln Arg Leu Gln Asp Ala Glu Ala Val Thr Ile Gly Lys Leu
241 245 250 255
244 Asn Met Asp Glu Phe Ala Met Gly Ser Ser Thr Glu Asn Ser Ala Tyr
245 260 265 270
248 Lys Leu Thr Lys Asn Pro Trp Asn Leu Asp Thr Val Pro Gly Gly Ser
249 275 280 285
252 Ser Gly Gly Ser Ala Ala Ala Val Ala Ala Gly Glu Val Pro Phe Ser
253 290 295 300
256 Leu Gly Ser Asp Thr Gly Gly Ser Ile Arg Gln Pro Ala Ser Phe Cys
257 305 310 315 320
260 Gly Val Val Gly Leu Lys Pro Thr Tyr Gly Arg Val Ser Arg Tyr Gly
261 325 330 335

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264 Leu Val Ala Phe Ala Ser Ser Leu Asp Gln Ile Gly Pro Ile Thr Arg
265           340           345           350
268 Thr Val Glu Asp Asn Ala Phe Leu Leu Gln Ala Ile Ser Gly Val Asp
269           355           360           365
272 Lys Met Asp Ser Thr Ser Ala Asn Val Asp Val Pro Asp Phe Leu Ser
273           370           375           380
276 Ser Leu Thr Gly Asp Ile Lys Gly Leu Lys Ile Ala Val Pro Lys Glu
277 385           390           395           400
280 Tyr Leu Gly Glu Gly Val Gly Lys Glu Ala Arg Glu Ser Val Leu Ala
281           405           410           415
284 Ala Leu Lys Val Leu Glu Gly Leu Gly Ala Thr Trp Glu Glu Val Ser
285           420           425           430
288 Leu Pro His Ser Lys Tyr Ala Leu Ala Thr Tyr Tyr Leu Leu Ser Ser
289           435           440           445
292 Ser Glu Ala Ser Ala Asn Leu Ala Arg Phe Asp Gly Ile Arg Tyr Gly
293           450           455           460
296 Tyr Arg Thr Asp Asn Ala Asp Asn Leu Ile Asp Leu Tyr Lys Gln Thr
297 465           470           475           480
300 Arg Ala Glu Gly Phe Gly Asn Glu Val Lys Arg Arg Ile Met Leu Gly
301           485           490           495
304 Thr Phe Ala Leu Ser Ser Gly Tyr Tyr Asp Ala Tyr Tyr Lys Lys Ala
305           500           505           510
308 Gln Lys Val Arg Thr Leu Ile Lys Lys Asp Phe Glu Asp Val Phe Glu
309           515           520           525
312 Lys Tyr Asp Val Ile Val Gly Pro Thr Thr Pro Thr Pro Ala Phe Lys
313           530           535           540
316 Ile Gly Glu Asn Thr Lys Asp Pro Leu Thr Met Tyr Ala Asn Asp Ile
317 545           550           555           560
320 Leu Thr Ile Pro Val Asn Leu Ala Ala Tyr Arg Glu Ser Gly Ala Met
321           565           570           575
324 Arg Leu Ala Asp Gly Leu Pro Leu Gly Leu Gln Ile Ile Gly Lys His
325           580           585           590
328 Phe Asp Glu Ala Leu Tyr Thr Ala Leu Leu Met His Leu Asn Lys Gln
329           595           600           605
332 Gln Thr Ile Ile Lys Gln Asn Leu Asn Cys Lys Gly Lys Glu Leu Asn
333           610           615           620
336 Phe Glu Thr Val Ile Gly Leu Glu Val His Val Glu Leu Lys Thr Lys
337 625           630           635           640
340 Ser Lys Ile Phe Ser Ser Ser Pro Thr Pro Phe Gly Ala Glu Ala Asn
341           645           650           655
344 Thr Gln Thr Ser Val Ile Asp Leu Gly Tyr Pro Gly Val Leu Pro Val
345           660           665           670
348 Leu Asn Lys Glu Ala Val Glu Phe Ala Met Lys Ala Ala Met Ala Leu
349           675           680           685
352 Asn Cys Glu Ile Ala Thr Asp Thr Lys Phe Asp Arg Lys Asn Tyr Phe
353           690           695           700
356 Tyr Pro Asp Asn Pro Lys Ala Tyr Gln Ile Ser Gln Phe Asp Lys Pro
357 705           710           715           720
360 Ile Gly Glu Asn Gly Trp Ile Glu Ile Glu Val Gly Gly Lys Thr Lys

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361          725          730          735
364 Arg Ile Gly Ile Thr Arg Leu His Leu Glu Glu Asp Ala Gly Lys Leu
365          740          745          750
368 Thr His Thr Gly Asp Gly Tyr Ser Leu Val Asp Phe Asn Arg Gln Gly
369          755          760          765
W--> 372 Thr Pro Leu Val Glu Xaa Val Ser Glu Pro Asp Ile Arg Thr Pro Glu
373          770          775          780
376 Glu Xaa Tyr Ala Tyr Leu Glu Lys Leu Lys Ser Ile Ile Gln Tyr Thr
377 785          790          795          800
380 Gly Val Ser Asp Cys Lys Met Glu Glu Gly Ser Leu Arg Cys Asp Ala
381          805          810          815
384 Asn Ile Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Lys Thr
385          820          825          830
388 Glu Leu Lys Asn Leu Asn Ser Phe Ala Phe Val Gln Lys Gly Leu Glu
389          835          840          845
392 His Glu Glu Lys Arg Gln Glu Gln Val Leu Leu Ser Gly Phe Phe Ile
393          850          855          860
396 Gln Gln Glu Thr Arg Arg Tyr Asp Glu Ala Thr Lys Lys Thr Ile Leu
397 865          870          875          880
400 Met Arg Val Lys Glu Gly Ser Asp Asp Tyr Arg Tyr Phe Pro Glu Pro
401          885          890          895
404 Asp Leu Val Glu Leu Tyr Ile Asp Asp Glu Trp Lys Glu Arg Val Lys
405          900          905          910
408 Ala Ser Ile Pro Glu Leu Pro Asp Glu Arg Arg Lys Arg Tyr Ile Glu
409          915          920          925
412 Glu Leu Gly Phe Ala Ala Tyr Asp Ala Met Val Leu Thr Leu Thr Lys
413          930          935          940
416 Glu Met Ala Asp Phe Phe Glu Glu Thr Val Gln Lys Gly Ala Glu Ala
417 945          950          955          960
420 Lys Gln Ala Ser Asn Trp Leu Met Gly Glu Val Ser Ala Tyr Leu Asn
421          965          970          975
424 Ala Glu Gln Lys Glu Leu Ala Asp Val Ala Leu Thr Pro Glu Gly Leu
425          980          985          990
428 Ala Gly Met Ile Lys Leu Ile Glu Lys Gly Thr Ile Ser Ser Lys Ile
429          995          1000          1005
432 Ala Lys Lys Val Phe Lys Glu Leu Ile Glu Lys Gly Gly Asp Ala
433          1010          1015          1020
436 Glu Lys Ile Val Lys Glu Lys Gly Leu Val Gln Ile Ser Asp Glu
437          1025          1030          1035
440 Gly Val Leu Leu Lys Leu Val Thr Glu Ala Leu Asp Asn Asn Pro
441          1040          1045          1050
444 Gln Ser Ile Glu Asp Phe Lys Asn Gly Lys Asp Arg Ala Ile Gly
445          1055          1060          1065
448 Phe Leu Val Gly Gln Ile Met Lys Ala Ser Lys Gly Gln Ala Asn
449          1070          1075          1080
452 Pro Pro Met Val Asn Lys Ile Leu Leu Glu Glu Ile Lys Lys Arg
453          1085          1090          1095
456 Lys Ser Ser Pro Arg Leu Leu Phe Leu Trp Ser Asn Asp Lys Asp
457          1100          1105          1110

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2330,2365 ✓

Seq#:2; Xaa Pos. 774,786 ✓

Seq#:5; N Pos. 455,490

Seq#:5; Xaa Pos. 152,164

Seq#:6; Xaa Pos. 152,164

## VERIFICATION SUMMARY

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L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2280  
M:341 Repeated in SeqNo=1  
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:768  
M:341 Repeated in SeqNo=2  
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:432  
M:341 Repeated in SeqNo=5  
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:144  
M:341 Repeated in SeqNo=6